

C. Remarks

The claims are 1-6, with claims 1 and 2 being independent.

Reconsideration of the present claims is expressly requested.

Claims 1-6 stand rejected under 35 U.S.C. § 102(b) as being allegedly anticipated by Mark Chee et al., "Accessing Generic Information with High-Density DNA Arrays," 274 Science 610-614 (1996) (Chee). The grounds of rejection are respectfully traversed.

Prior to addressing the merits of rejection, Applicants again would like to briefly review some of the key features and advantages of the presently claimed invention. In the present invention, plural template patterns are obtained using a probe array and nucleic acids complementary to the probes. A sample hybridization pattern is obtained using the probe array, and a test sample is compared with the above-mentioned template patterns. When there is a substantial identity between the test sample and one of the template patterns, it is determined that the test nucleic acid sequence has a sequence portion identical to the nucleic acid that produced the identical template pattern. The presently claimed method enables an accurate identification of a sequence without disposing a vast number of probes of all-inclusive sequences.

Applicants respectfully submit that Chee does not disclose or suggest carrying out sequence identification by comparing a pattern of fluorescent intensity obtained using a sample nucleic acid with plural template patterns obtained using nucleic acids of known sequences to determine a match in the presently claimed manner. Chee only teaches comparing a fluorescent pattern obtained using a mutant sample with a fluorescent pattern obtained using a standard sample.

Chee teaches on page 612, columns 2 and 3, and in Fig. 3 that a fluorescent pattern with mt3 and patterns of LHON4216, LHON 13708 were obtained, which Applicants believe is the portion of Chee that the Examiner has alleged to represent step (d) in the presently claimed invention. Chee, however, does not disclose or suggest using plural template patterns for identification by comparison.

The DNA chip in Chee is a 4L tilted array where a vast number of probes, designated to have one base mismatch for every base position of a standard sequence, are arranged. Analysis of the obtained hybridization pattern with a sample nucleic acid enables an easy identification of a single base mutation, i.e., when the pattern obtained with a sample is different from the standard pattern, the base change can be directly read from the different intensities of the four probes having A, T, G or C at that corresponding site. Thus, Applicants submit that Chee does not disclose or suggest preparation of plural template patterns to serve as a reference dictionary from which the pattern matching the hybridization pattern of a sample nucleic acid can be identified. This feature, as presently claimed, is especially effective when the mismatch base positions are located in close proximity to each other (see substitute specification, paragraph [0027]).

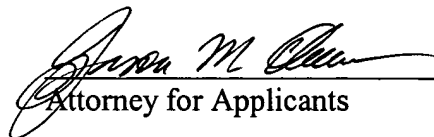
The Examiner has alleged that when one pattern is compared with another pattern, the patterns match or they do not match. If the patterns match, they are the same. If the patterns do not match, they are different. This argument is only valid, however, when there is a one-to-one relationship between the template pattern and the sample pattern. As discussed above, however, the presently claimed use of plural template patterns is neither disclosed nor suggested by Chee.

Thus, if the present inventive method were applied to Chee, for example, four sets of probes for mit1 (3), LHON3460, LHON4216 and LHON13708 would be prepared and immobilized on one chip, and four template patterns would be obtained by hybridizing each of the nucleic acids. Then, a test nucleic acid would be hybridized to the chip containing four probe sets, and the obtained hybridization pattern would be compared with four template patterns to identify the sample nucleic acid to be either mit1 (3), LHON3460, LHON4216 or LHON13708. Applicants respectfully submit that this is not how Chee teaches to identify a test sample.

In conclusion, Applicants respectfully submit that it is clear that Chee does not disclose or suggest using plural template patterns as presently claimed. Thus, Chee cannot affect the patentability of the presently claimed invention. Wherefore, it is respectfully requested that the outstanding rejection be withdrawn and the present case be passed to issue.

Applicants' undersigned attorney may be reached in our New York office by telephone at (212) 218-2100. All correspondence should continue to be directed to our below listed address.

Respectfully submitted,


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